

SEQUENCE LISTING

<110> Hemmati-Brivanlou, Ali  
Weinstein, Daniel C.

<120> TRANSLATION INITIATION FACTOR 4AIII, AND METHODS OF USE  
THEREOF

<130> 600-1-211 N

<140> UNASSIGNED  
<141> 1999-05-25

<160> 12

<170> PatentIn Ver. 2.0

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<211> 1245  
<212> DNA  
<213> Xenopus laevis

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cagtgtttgg atattcagat ccgtgaaacc caagccttga ttttagcacc caccaaagag 360  
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<210> 2  
<211> 415  
<212> PRT

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260 265 270

Asp Leu Tyr Asp Thr Leu Thr Ile Thr Gln Ala Val Ile Phe Cys Asn  
275 280 285

Thr Lys Arg Lys Val Asp Trp Leu Thr Glu Lys Met Arg Glu Ala Asn  
290 295 300

Phe Thr Val Ser Ser Met His Gly Asp Met Pro Gln Lys Glu Arg Glu  
305 310 315 320

Ser Ile Met Lys Glu Phe Arg Ser Gly Ala Ser Arg Val Leu Ile Ser  
325 330 335

Thr Asp Val Trp Ala Arg Gly Leu Asp Val Pro Gln Val Ser Leu Ile  
340 345 350

Ile Asn Tyr Asp Leu Pro Asn Asn Arg Glu Leu Tyr Ile His Arg Ile  
355 360 365

Gly Arg Ser Gly Arg Tyr Gly Arg Lys Gly Val Ala Ile Asn Phe Val  
370 375 380

Lys Asn Asp Asp Ile Arg Ile Leu Arg Asp Ile Glu Gln Tyr Tyr Ser  
385 390 395 400

Thr Gln Ile Asp Glu Met Pro Met Asn Val Ala Asp Leu Ile Glx  
405 410 415

<210> 3

<211> 532

<212> DNA

<213> Homo sapiens

<400> 3

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ttgatcttgg ctcccacaag agagttggct gtgcagatcc agaaggggct gcttgctctc 180  
ggtgactaca tgaatgtcca gtgccatgcc tgcattggag gcaccaatgt tggcgaggac 240  
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gtgaaatgt tgaataaagg tttcaaagag cagatttacg atgtatacag gtacctgcct 420  
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<213> Xenopus laevis

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Ala Lys Arg Leu Leu Arg Glu Glu Asp Met Thr Thr Val Glu Phe Gln  
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Thr Ser Glu Glu Val Asp Val Thr Pro Thr Phe Asp Thr Met Gly Leu  
35 40 45

Arg Glu Asp Leu Leu Arg Gly Ile Tyr Ala Tyr Gly Phe Glu Lys Pro  
50 55 60

Ser Ala Ile Gln Gln Lys Ala Ile Lys Gln Ile Ile Lys Gly Arg Asp  
65 70 73 75 80

Val Ile Ala Gln Ser Gln Ser Gly Thr Gly Lys Thr Ala Thr Phe Cys  
85 90 95

Ile Val Ser Val Leu Gln Cys Leu Asp Ile Gln Ile Arg Glu Thr Gln Ala  
100 105 110

Leu Ile Leu Ala Pro Thr Lys Glu Leu Ala Arg Gln Ile Gln Lys Val  
115 120 125

Leu Leu Ala Leu Gly Asp Tyr Met Asn Val Gln Cys His Ala Cys Ile  
130 135 140

Gly Gly Thr Asn Val Gly Glu Asp Ile Arg Lys Leu Asp Tyr Gly Gln  
145 150 155 160

His Val Val Ala Gly Thr Pro Gly Arg Val Phe Asp Met Ile Arg Arg  
165 170 175

Arg Ser Leu Arg Thr Arg Ala Ile Lys Met Leu Val Leu Asp Glu Ala  
180 185 190

Asp Glu Met Leu Asn Lys Gly Phe Lys Glu Gln Ile Tyr Asp Val Tyr  
195 200 205

Arg Tyr Leu Pro Pro Ala Thr Gln Val Cys Leu Ile Ser Ala Thr Leu  
210 215 220

Pro His Glu Ile Leu Glu Met Thr Asn Lys Phe Met Thr Asp Pro Ile  
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532

<210> 4

<211> 177

<212> PRT

<213> Homo sapiens

<400> 4

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20 25 30

Ile Gln Val Arg Glu Thr Gln Ala Leu Ile Leu Ala Pro Thr Arg Glu  
35 40 45

Leu Ala Val Gln Ile Gln Lys Gly Leu Leu Ala Leu Gly Asp Tyr Met  
50 55 60

Asn Val Gln Cys His Ala Cys Ile Gly Gly Thr Asn Val Gly Glu Asp  
65 70 75 80

Ile Arg Lys Leu Asp Tyr Gly Gln His Val Val Ala Gly Thr Pro Gly  
85 90 95

Arg Val Phe Asp Met Ile Arg Arg Arg Ser Leu Arg Thr Arg Ala Ile  
100 105 110

Lys Met Leu Val Leu Asp Glu Ala Asp Glu Met Leu Asn Lys Gly Phe  
115 120 125

Lys Glu Gln Ile Tyr Asp Val Tyr Arg Tyr Leu Pro Pro Ala Thr Gln  
130 135 140

Val Val Leu Ile Ser Ala Thr Leu Pro His Glu Ile Leu Glu Met Thr  
145 150 155 160

Asn Lys Phe Met Thr Asp Pro Ile Arg Ile Leu Val Gly Ile Pro Ala  
165 170 175

Ala

<210> 5

<211> 1536

<212> DNA

<213> Homo sapiens

<400> 5

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gctgctcaaa gaggaagaca tgactaaagt ggaattcgag accagcgagg aggtggatgt 180  
gaccccccacg ttgcacacca tgggcctcg gggggacctg ctgcgggca tctacgctta 240  
cggtttgaa aaaccatcg caatccagca acgagcaatc aagcagatca tcaaaggagg 300  
agatgtcatc gcacagtctc agtccggcac agaaaaaca gccaccctca gtatctca 360  
cctccagtgt ttggatattc aggttcgtga aactcaagct ttgatcttgg ctcccacaag 420  
agagttggct gtgcagatcc agaagggct gcttgctctc ggtgactaca tgaatgtcca 480  
gtgccatgcc tgcattggag gcaccaatgt tggcgaggac atcagaagc tggattacgg 540  
acagcatgtt gtcgcgggca ctccaggcg tggatgtt atgattcgtc gcagaaggct 600  
aaggacacgt gctatcaaaa tggatgttt ggatgaagct gatgaaatgt tgaataaaagg 660  
tttcaaagag cagattacg atgtatacag gtacctgcct tcagccacac aggtggttct 720  
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aatccgcattc ttggtaaac gtgatgaatt gactctggaa ggcataaagc aattttctgt 840  
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catcactcag gcggcatct tctgcaacac caaaagaaag gtggactggc tgacggagaa 960  
aatgagggaa gccaacttca ctgtatctc aatgcatgga gacatgcccc agaaagagcg 1020  
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gattctactt aatggggttt atatggactt tcttctcata aatggcctgc cgtctccctt 1440  
cctttaaga ggatatgggg attctgcctt ctttcttat ttacatgtaa ataatacatt 1500  
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<210> 6

<211> 411

<212> PRT

<213> Homo sapiens

<400> 6

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20 25 30

Glu Val Asp Val Thr Pro Thr Phe Asp Thr Met Gly Leu Arg Glu Asp  
35 40 45

Leu Leu Arg Gly Ile Tyr Ala Tyr Gly Phe Glu Lys Pro Ser Ala Ile  
50 55 60

Gln Gln Arg Ala Ile Lys Gln Ile Ile Lys Gly Arg Asp Val Ile Ala  
65 70 75 80

Gln Ser Gln Ser Gly Thr Gly Lys Thr Ala Thr Phe Ser Ile Ser Val  
85 90 95

Leu Gln Cys Leu Asp Ile Gln Val Arg Glu Thr Gln Ala Leu Ile Leu  
100 105 110

Ala Pro Thr Arg Glu Leu Ala Val Gln Ile Gln Lys Gly Leu Leu Ala  
115 120 125

Leu Gly Asp Tyr Met Asn Val Gln Cys His Ala Cys Ile Gly Gly Thr  
130 135 140

Asn Val Gly Glu Asp Ile Arg Lys Leu Asp Tyr Gly Gln His Val Val  
145 150 155 160

Ala Gly Thr Pro Gly Arg Val Phe Asp Met Ile Arg Arg Arg Ser Leu  
165 170 175

Arg Thr Arg Ala Ile Lys Met Leu Val Leu Asp Glu Ala Asp Glu Met  
180 185 190

Leu Asn Lys Gly Phe Lys Glu Gln Ile Tyr Asp Val Tyr Arg Tyr Leu  
195 200 205

Pro Ser Ala Thr Gln Val Val Leu Ile Ser Ala Thr Leu Pro His Glu  
210 215 220

Ile Leu Glu Met Thr Asn Lys Phe Met Thr Asp Pro Ile Arg Ile Leu  
225 230 235 240

Val Lys Arg Asp Glu Leu Thr Leu Glu Gly Ile Lys Gln Phe Phe Val  
245 250 255

Ala Val Glu Arg Glu Glu Trp Lys Phe Asp Thr Leu Cys Asp Leu Tyr  
260 265 270

Asp Thr Leu Thr Ile Thr Gln Ala Val Ile Phe Cys Asn Thr Lys Arg  
275 280 285

Lys Val Asp Trp Leu Thr Glu Lys Met Arg Glu Ala Asn Phe Thr Val  
290 295 300

Ser Ser Met His Gly Asp Met Pro Gln Lys Glu Arg Glu Ser Ile Met  
305 310 315 320

Lys Glu Phe Arg Ser Gly Ala Ser Arg Val Leu Ile Ser Thr Asp Val

325

330

335

Trp Ala Arg Gly Leu Asp Val Pro Gln Val Ser Leu Ile Ile Asn Tyr

340

345

350

Asp Leu Pro Asn Asn Arg Glu Leu Tyr Ile His Arg Ile Gly Arg Ser

355

360

365

Gly Gln Tyr Gly Arg Lys Gly Val Ala Ile Asn Phe Val Lys Asn Asp

370

375

380

Asp Ile Arg Ile Leu Arg Asp Ile Glu Gln Tyr Tyr Ser Thr Gln Ile

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390

395

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Asp Glu Met Pro Met Asn Val Ala Asp Leu Ile

405

410

<210> 7

<211> 1682

<212> DNA

<213> Homo sapiens

<400> 7

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ctcgggctcg ggcgaaagc ggctgctcaa agaggaagac atgactaaag tggattcga 300  
gaccagcgag gaggtggatg tgaccccac gttcgacacc atgggcctgc gggaggac 360  
gctgcggggc atctacgctt acggtttga aaaaccatca gcaatccagc aacgagcaat 420  
caagcagatc atcaaaggga gagatgtcat cgcacagtct cagtccggca caggaaaaac 480  
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cggtgactac atgaatgtcc agtgcctgc ctgcatttgc ggcaccaatg ttggcgagga 660  
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tatgattcgt cgcagaagcc taaggacacg tgctatcaaa atgttggttt tggatgaagc 780  
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at 1682

<210> 8  
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<212> PRT  
<213> Homo sapiens

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Glu Val Asp Val Thr Pro Thr Phe Asp Thr Met Gly Leu Arg Glu Asp  
35 40 45  
  
Leu Leu Arg Gly Ile Tyr Ala Tyr Gly Phe Glu Lys Pro Ser Ala Ile  
50 55 60  
  
Gln Gln Arg Ala Ile Lys Gln Ile Ile Lys Gly Arg Asp Val Ile Ala  
65 70 75 80  
  
Gln Ser Gln Ser Gly Thr Gly Lys Thr Ala Thr Phe Ser Ile Ser Val  
85 90 95  
  
Leu Gln Cys Leu Asp Ile Gln Val Arg Glu Thr Gln Ala Leu Ile Leu  
100 105 110  
  
Ala Pro Thr Arg Glu Leu Ala Val Gln Ile Gln Lys Gly Leu Leu Ala  
115 120 125  
  
Leu Gly Asp Tyr Met Asn Val Gln Cys His Ala Cys Ile Gly Gly Thr  
130 135 140  
  
Asn Val Gly Glu Asp Ile Arg Lys Leu Asp Tyr Gly Gln His Val Val  
145 150 155 160  
  
Ala Gly Thr Pro Gly Arg Val Phe Asp Met Ile Arg Arg Arg Ser Leu  
165 170 175  
  
Arg Thr Arg Ala Ile Lys Met Leu Val Leu Asp Glu Ala Asp Glu Met  
180 185 190

Leu Asn Lys Gly Phe Lys Glu Gln Ile Tyr Asp Val Tyr Arg Tyr Leu  
195 200 205

Pro Pro Ala Thr Gln Val Val Leu Ile Ser Ala Thr Leu Pro His Glu  
210 215 220

Ile Leu Glu Met Thr Asn Lys Phe Met Thr Asp Pro Ile Arg Ile Leu  
225 230 235 240

Val Lys Arg Asp Glu Leu Thr Leu Glu Gly Ile Lys Gln Phe Phe Val  
245 250 255

Ala Val Glu Arg Glu Glu Trp Lys Phe Asp Thr Leu Cys Asp Leu Tyr  
260 265 270

Asp Thr Leu Thr Ile Thr Gln Ala Val Ile Phe Cys Asn Thr Lys Arg  
275 280 285

Lys Val Asp Trp Leu Thr Glu Lys Met Arg Glu Ala Asn Phe Thr Val  
290 295 300

Ser Ser Met His Gly Asp Met Pro Gln Lys Glu Arg Glu Ser Ile Met  
305 310 315 320

Lys Glu Phe Arg Ser Gly Ala Ser Arg Val Leu Ile Ser Thr Asp Val  
325 330 335

Trp Ala Arg Gly Leu Asp Val Pro Gln Val Ser Leu Ile Ile Asn Tyr  
340 345 350

Asp Leu Pro Asn Asn Arg Glu Leu Tyr Ile His Arg Ile Gly Arg Ser  
355 360 365

Gly Arg Tyr Gly Arg Lys Gly Val Ala Ile Asn Phe Val Lys Asn Asp  
370 375 380

Asp Ile Arg Ile Leu Arg Asp Ile Glu Gln Tyr Tyr Ser Thr Gln Ile  
385 390 395 400

Asp Glu Met Pro Met Asn Val Ala Asp Leu Ile  
405 410

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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

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gggtgttgcc attaactttg tc 22

<210> 10  
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<400> 10  
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<210> 11  
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<212> DNA  
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<223> Description of Artificial Sequence:primer

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<210> 12  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

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tggaatgttag ccagtctgcc 20